



## SEQUENCE LISTING

<110> Meyers, Rachel A.

<120> 26583, A NOVEL SERINE/THREONINE  
PHOSPHATASE AND USES THEREFOR

<130> 10448-025001

<150> US 60/187,454

<151> 2000-03-07

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2838

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (462)...(2072)

<221> misc\_feature

<222> (1)...(2838)

<223> n = A,T,C or G

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ttttgtcttt tatttcaagg tcccggatcc ggtggtggtg caaatcaaa aactgctcct      180
cagtggatgt tgcctttact tctaggcctg tacggaagtg ttacttctgc tctaaaagct      240
gcggaattct aatacgactc actataggga gtcgaccac gcgtccggtg ggcaggccgg      300
gggtgagggc tcgctgctcc ggagctgcac ggggctgcgt ggaaagagcg ccgagcgggtg      360
gcgtcgttgt cgtccctctc tcgtcgggaa gaatcgtttg gtctcctgcc gtgcccggaa      420
tcccagtcag aagttccagc ctgccactgt tctctgatgc c atg cca gca cca act      476
                                         Met Pro Ala Pro Thr
                                         1             5
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caa ctg ttt ttt cct ctc atc cgt aac tgt gaa ctg agc agg atc tat      524
Gln Leu Phe Phe Pro Leu Ile Arg Asn Cys Glu Leu Ser Arg Ile Tyr
                        10                        15                        20
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ggc act gca tgt tac tgc cac cac aaa cat ctc tgt tgt tcc tca tcg      572
Gly Thr Ala Cys Tyr Cys His His Lys His Leu Cys Cys Ser Ser Ser
                        25                        30                        35
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tac att cct cag agt cga ctg aga tac aca cct cat cca gca tat gct      620
Tyr Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro His Pro Ala Tyr Ala
                        40                        45                        50
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acc ttt tgc agg cca aag gag aac tgg tgg cag tac acc caa gga agg      668
Thr Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln Tyr Thr Gln Gly Arg
                        55                        60                        65
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aga tat gct tcc aca cca cag aaa ttt tac ctc aca cct cca caa gtc      716
Arg Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu Thr Pro Pro Gln Val
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09801267 070901 106070 2970360

70	75	80	85	
aat agc atc ctt aaa gct aat gaa tac agt ttc aaa gtg cca gaa ttt				764
Asn Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe Lys Val Pro Glu Phe				
	90	95	100	
gac ggc aaa aat gtc agt tct atc ctt gga ttt gac agc aat cag ctg				812
Asp Gly Lys Asn Val Ser Ser Ile Leu Gly Phe Asp Ser Asn Gln Leu				
	105	110	115	
cct gca aat gca ccc att gag gac cgg aga agt gca gca acc tgc ttg				860
Pro Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser Ala Ala Thr Cys Leu				
	120	125	130	
cag acc aga ggg atg ctt ttg ggg gtt ttt gat ggc cat gca ggt tgt				908
Gln Thr Arg Gly Met Leu Leu Gly Val Phe Asp Gly His Ala Gly Cys				
	135	140	145	
gct tgt tcc cag gca gtc agt gaa aga ctc ttt tat tat att gct gtc				956
Ala Cys Ser Gln Ala Val Ser Glu Arg Leu Phe Tyr Tyr Ile Ala Val				
	150	155	160	165
tct ttg tta ccc cat gag act ttg cta gag att gaa aat gca gtg gag				1004
Ser Leu Leu Pro His Glu Thr Leu Leu Glu Ile Glu Asn Ala Val Glu				
	170	175	180	
agc ggc cgg gca ctg cta ccc att ctc cag tgg cac aag cac ccc aat				1052
Ser Gly Arg Ala Leu Leu Pro Ile Leu Gln Trp His Lys His Pro Asn				
	185	190	195	
gat tac ttt agt aag gag gca tcc aaa ttg tac ttt aac agc ttg agg				1100
Asp Tyr Phe Ser Lys Glu Ala Ser Lys Leu Tyr Phe Asn Ser Leu Arg				
	200	205	210	
act tac tgg caa gag ctt ata gac ctc aac act ggt gag tcg act gat				1148
Thr Tyr Trp Gln Glu Leu Ile Asp Leu Asn Thr Gly Glu Ser Thr Asp				
	215	220	225	
att gat gtt aag gag gct cta att aat gcc ttc aag agg ctt gat aat				1196
Ile Asp Val Lys Glu Ala Leu Ile Asn Ala Phe Lys Arg Leu Asp Asn				
	230	235	240	245
gac atc tcc ttg gag gcg caa gtt ggt gat cct aat tct ttt ctc aac				1244
Asp Ile Ser Leu Glu Ala Gln Val Gly Asp Pro Asn Ser Phe Leu Asn				
	250	255	260	
tac ctg gtg ctt cga gtg gca ttt tct gga gcc act gct tgt gtg gcc				1292
Tyr Leu Val Leu Arg Val Ala Phe Ser Gly Ala Thr Ala Cys Val Ala				
	265	270	275	
cat gtg gat ggt gtt gac ctt cat gtg gcc aat act ggc gat agc aga				1340
His Val Asp Gly Val Asp Leu His Val Ala Asn Thr Gly Asp Ser Arg				
	280	285	290	
gcc atg ctg ggt gtg cag gaa gag gac ggc tca tgg tca gca gtc acg				1388
Ala Met Leu Gly Val Gln Glu Glu Asp Gly Ser Trp Ser Ala Val Thr				
	295	300	305	
ctg tct aat gac cac aat gct caa aat gaa aga gaa cta gaa cgg ctg				1436
Leu Ser Asn Asp His Asn Ala Gln Asn Glu Arg Glu Leu Glu Arg Leu				
	310	315	320	325

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aaa ttg gaa cat cca aag agt gag gcc aag agt gtc gtg aaa cag gat 1484  
 Lys Leu Glu His Pro Lys Ser Glu Ala Lys Ser Val Val Lys Gln Asp  
 330 335 340

cgg ctg ctt ggc ttg ctg atg cca ttt agg gca ttt gga gat gta aag 1532  
 Arg Leu Leu Gly Leu Leu Met Pro Phe Arg Ala Phe Gly Asp Val Lys  
 345 350 355

ttc aaa tgg agc att gac ctt caa aag aga gtg ata gaa tct ggc cca 1580  
 Phe Lys Trp Ser Ile Asp Leu Gln Lys Arg Val Ile Glu Ser Gly Pro  
 360 365 370

gac cag ttg aat gac aat gaa tat acc aag ttt att cct cct aat tat 1628  
 Asp Gln Leu Asn Asp Asn Glu Tyr Thr Lys Phe Ile Pro Pro Asn Tyr  
 375 380 385

cac aca cct cct tat ctc act gct gag cca gag gta act tac cac cga 1676  
 His Thr Pro Pro Tyr Leu Thr Ala Glu Pro Glu Val Thr Tyr His Arg  
 390 395 400 405

tta agg cca cag gat aag ttt ctg gtg ttg gct act gat ggg ttg tgg 1724  
 Leu Arg Pro Gln Asp Lys Phe Leu Val Leu Ala Thr Asp Gly Leu Trp  
 410 415 420

gag act atg cat agg cag gat gtg gtt agg att gtg ggt gag tac cta 1772  
 Glu Thr Met His Arg Gln Asp Val Val Arg Ile Val Gly Glu Tyr Leu  
 425 430 435

act ggc atg cat cac caa cag cca ata gct gtt ggt ggc tac aag gtg 1820  
 Thr Gly Met His His Gln Gln Pro Ile Ala Val Gly Gly Tyr Lys Val  
 440 445 450

act ctg gga cag atg cat ggc ctt tta aca gaa agg aga acc aaa atg 1868  
 Thr Leu Gly Gln Met His Gly Leu Leu Thr Glu Arg Arg Thr Lys Met  
 455 460 465

tcc tcg gta ttt gag gat cag aac gca gca acc cat ctc att cgc cac 1916  
 Ser Ser Val Phe Glu Asp Gln Asn Ala Ala Thr His Leu Ile Arg His  
 470 475 480 485

gct gtg ggc aac aac gag ttt ggg act gtt gat cat gag cgc ctc tct 1964  
 Ala Val Gly Asn Asn Glu Phe Gly Thr Val Asp His Glu Arg Leu Ser  
 490 495 500

aaa atg ctt agt ctt cct gaa gag ctt gct cga atg tac aga gat gac 2012  
 Lys Met Leu Ser Leu Pro Glu Glu Leu Ala Arg Met Tyr Arg Asp Asp  
 505 510 515

att aca atc att gta gtt cag ttc aat tct cat gtt gta ggg gcg tat 2060  
 Ile Thr Ile Ile Val Val Gln Phe Asn Ser His Val Val Gly Ala Tyr  
 520 525 530

caa aac caa gaa tagtgagtgg ctctttcact ggcaattctc aaatgatata 2112  
 Gln Asn Gln Glu  
 535

catttaaagg gcagattttt taaaaagata ctactataat aaacatttcc agttgggtcat 2172  
 tctaagcatt tacccttttg atactctagc tagtcaggta ctocaaattg actttgcagc 2232  
 aggggtggcag gggtcaggaga gtctgggtcct gcctagctca gattttcatgg cacctgcact 2292  
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agaaaattag gatgacctgg caaataagat cttgaatagg ccaaaagcaa gtatcttgct 2412
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ttccagtgtg catgagaaca tatatttatt ksmwkrwttt yywrrtacac agtctatgca 2532
ttwttcataw wmauttattt twgcctaaat aargtkkttw wcamatcyag tthwtcmatc 2592
matraacras mamcaascaa tctrtatktr tttttkktkw trwttrwytg rmakgmwtsy 2652
twaktrrrak ramtawmcwc mstyatccay ccgmyykmyt wmykwaaktr attgaaatat 2712
tttttwtttt gccccccctt tggagtcaag aagggttttt agtttttatct tctyttctat 2772
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<210> 2
<211> 537
<212> PRT
<213> Homo sapiens

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Cys Cys Ser Ser Ser Tyr Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro
35 40 45
His Pro Ala Tyr Ala Thr Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln
50 55 60
Tyr Thr Gln Gly Arg Arg Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu
65 70 75 80
Thr Pro Pro Gln Val Asn Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe
85 90 95
Lys Val Pro Glu Phe Asp Gly Lys Asn Val Ser Ser Ile Leu Gly Phe
100 105 110
Asp Ser Asn Gln Leu Pro Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser
115 120 125
Ala Ala Thr Cys Leu Gln Thr Arg Gly Met Leu Leu Gly Val Phe Asp
130 135 140
Gly His Ala Gly Cys Ala Cys Ser Gln Ala Val Ser Glu Arg Leu Phe
145 150 155 160
Tyr Tyr Ile Ala Val Ser Leu Leu Pro His Glu Thr Leu Leu Glu Ile
165 170 175
Glu Asn Ala Val Glu Ser Gly Arg Ala Leu Leu Pro Ile Leu Gln Trp
180 185 190
His Lys His Pro Asn Asp Tyr Phe Ser Lys Glu Ala Ser Lys Leu Tyr
195 200 205
Phe Asn Ser Leu Arg Thr Tyr Trp Gln Glu Leu Ile Asp Leu Asn Thr
210 215 220
Gly Glu Ser Thr Asp Ile Asp Val Lys Glu Ala Leu Ile Asn Ala Phe
225 230 235 240
Lys Arg Leu Asp Asn Asp Ile Ser Leu Glu Ala Gln Val Gly Asp Pro
245 250 255
Asn Ser Phe Leu Asn Tyr Leu Val Leu Arg Val Ala Phe Ser Gly Ala
260 265 270
Thr Ala Cys Val Ala His Val Asp Gly Val Asp Leu His Val Ala Asn
275 280 285
Thr Gly Asp Ser Arg Ala Met Leu Gly Val Gln Glu Glu Asp Gly Ser
290 295 300
Trp Ser Ala Val Thr Leu Ser Asn Asp His Asn Ala Gln Asn Glu Arg
305 310 315 320
Glu Leu Glu Arg Leu Lys Leu Glu His Pro Lys Ser Glu Ala Lys Ser
325 330 335
Val Val Lys Gln Asp Arg Leu Leu Gly Leu Leu Met Pro Phe Arg Ala
340 345 350
Phe Gly Asp Val Lys Phe Lys Trp Ser Ile Asp Leu Gln Lys Arg Val

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355 360 365  
 Ile Glu Ser Gly Pro Asp Gln Leu Asn Asp Asn Glu Tyr Thr Lys Phe  
 370 375 380  
 Ile Pro Pro Asn Tyr His Thr Pro Pro Tyr Leu Thr Ala Glu Pro Glu  
 385 390 395 400  
 Val Thr Tyr His Arg Leu Arg Pro Gln Asp Lys Phe Leu Val Leu Ala  
 405 410 415  
 Thr Asp Gly Leu Trp Glu Thr Met His Arg Gln Asp Val Val Arg Ile  
 420 425 430  
 Val Gly Glu Tyr Leu Thr Gly Met His His Gln Gln Pro Ile Ala Val  
 435 440 445  
 Gly Gly Tyr Lys Val Thr Leu Gly Gln Met His Gly Leu Leu Thr Glu  
 450 455 460  
 Arg Arg Thr Lys Met Ser Ser Val Phe Glu Asp Gln Asn Ala Ala Thr  
 465 470 475 480  
 His Leu Ile Arg His Ala Val Gly Asn Asn Glu Phe Gly Thr Val Asp  
 485 490 495  
 His Glu Arg Leu Ser Lys Met Leu Ser Leu Pro Glu Glu Leu Ala Arg  
 500 505 510  
 Met Tyr Arg Asp Asp Ile Thr Ile Ile Val Val Gln Phe Asn Ser His  
 515 520 525  
 Val Val Gly Ala Tyr Gln Asn Gln Glu  
 530 535

<210> 3  
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 <212> DNA  
 <213> Homo sapiens

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 cagagtcgac tgagatacac acctcatcca gcatatgcta cctttttgcag gccaaaggag 180  
 aactggtggc agtacaccca aggaaggaga tatgcttcca caccacagaa attttacctc 240  
 acacctccac aagtcaatag catccttaaa gctaataaat acagtttcaa agtgccagaa 300  
 tttagcggca aaaatgtcag ttctatcctt ggatttgaca gcaatcagct gcctgcaaat 360  
 gcacccattg aggaccggag aagtgcagca acctgcttgc agaccagagg gatgcttttg 420  
 ggggtttttg atggccatgc aggttgtgct tgttcccagg cagtcagtga aagactcttt 480  
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 gagagcggcc gggcactgct acccattctc cagtggcaca agcaccceaa tgattacttt 600  
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 tataccaagt ttattcctcc taattatcac acacctcctt atctcactgc tgagccagag 1200  
 gtaacttacc accgattaag gccacaggat aagtttcttg tgttggtac tgatgggttg 1260  
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 cttttaacag aaaggagaac caaaatgtcc tcggtatttg aggatcagaa cgcagcaacc 1440  
 catctcattc gccacgctgt gggcaacaac gagtttggga ctgttgatca tgagcgcttc 1500  
 tctaaaatgc ttagtcttcc tgaagagctt gctcgaatgt acagagatga cattacaatc 1560  
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<210> 4  
 <211> 300  
 <212> PRT

09801267.070901

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 4

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			20					25					30		
Asp	Ser	Trp	Ser	Phe	Phe	Ala	Val	Phe	Asp	Gly	His	Gly	Ser	Gln	Ala
		35					40					45			
Ala	Lys	Tyr	Ala	Gly	Lys	His	Leu	His	Lys	Thr	Ile	Leu	Ala	Glu	Arg
	50					55					60				
Lys	Ser	Phe	Pro	Glu	Gly	Asp	Pro	Trp	Glu	Met	Lys	Leu	Ser	Asp	Leu
65				70					75					80	
Glu	Asp	Ala	Leu	Lys	Glu	Ser	Phe	Leu	Glu	Ala	Asp	Thr	Asp	Glu	Glu
			85						90					95	
Leu	Arg	Ser	Ala	Glu	Ala	Ser	Ala	Ala	Asn	Lys	Val	Leu	Thr	Lys	Glu
			100					105						110	
Asp	Leu	Ser	Ser	Gly	Ser	Thr	Ala	Val	Val	Ala	Leu	Ile	Arg	Gly	Asn
		115					120						125		
Lys	Leu	Tyr	Val	Ala	Asn	Val	Gly	Asp	Ser	Arg	Ala	Val	Leu	Cys	Arg
	130					135					140				
Asn	Gly	Asn	Ala	Ile	Lys	Trp	Ala	Val	Thr	Leu	Thr	Glu	Asp	His	Lys
145					150					155				160	
Pro	Ser	Asn	Glu	Asp	Glu	Arg	Glu	Arg	Ile	Glu	Ala	Ala	Gly	Gly	Phe
			165						170					175	
Val	Ser	Arg	Val	Ser	Asn	Gly	Arg	Val	Asn	Gly	Val	Leu	Ala	Val	Ser
			180					185						190	
Arg	Ala	Phe	Gly	Asp	Phe	Glu	Leu	Lys	Pro	Gly	Ser	Lys	Leu	Gly	Pro
		195					200					205			
Glu	Glu	Ser	Leu	Glu	Ala	Asn	Tyr	Glu	Tyr	Ile	Lys	Ser	Pro	Glu	Gln
	210					215					220				
Leu	Val	Thr	Ala	Glu	Pro	Asp	Val	Thr	Ser	Ser	Thr	Asp	Leu	Thr	Pro
225					230					235				240	
Asp	Lys	Asp	Glu	Phe	Leu	Ile	Leu	Ala	Cys	Asp	Gly	Leu	Trp	Asp	Val
			245						250					255	
Val	Ser	Asp	Gln	Glu	Val	Val	Asp	Ile	Val	Arg	Ser	Glu	Leu	Ser	Asp
			260					265					270		
Gly	Asn	Lys	Ser	Ala	Glu	Asp	Pro	Met	Glu	Ala	Ala	Glu	Lys	Leu	Val
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<210> 5

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 5

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		20						25					30		
Pro	Phe	Phe	Gly	Val	Phe	Asp	Gly	His	Gly	Gly	Ser	Glu	Ala	Ala	Lys
		35					40					45			
Phe	Leu	Ser	Lys	Asn	Leu	His	Glu	Ile	Leu	Ala	Glu	Glu	Leu	Ser	Phe

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50		55		60
Asp Lys Asp Glu Ser Leu Lys Glu Asn Glu Glu Leu Lys Asp Glu Pro				
65		70		75
Glu Ser Ser Glu Arg Leu Asn Gly Asp Lys Ser Leu Glu Asp Val Glu				80
	85		90	95
Glu Ala Leu Arg Lys Ala Phe Leu Arg Thr Asp Glu Glu Ile Ser Thr				
	100		105	110
Ala Val Val Ala Leu Ile Arg Gly Asn Lys Leu Tyr Val Ala Asn Val				
	115		120	125
Gly Asp Ser Arg Ala Val Leu Cys Arg Asn Gly Lys Asp Ser Trp Glu				
	130		135	140
Gly Val Arg Thr Tyr Ser Ala Val Gln Leu Thr Glu Asp His Lys Pro				
145		150		155
Ser Asn Glu Asp Glu Arg Glu Arg Ile Glu Ala Ala Gly Gly Glu Val				160
	165		170	175
Glu Pro Ile Asp Arg Glu Phe Val Ser Asn Gly Gly Gly Val Val Trp				
	180		185	190
Arg Val Asn Gly Val Val Ile Ser Leu Ala Val Ser Arg Ala Leu Gly				
	195		200	205
Asp Phe Glu Leu Lys Lys Lys Glu Asp Glu Leu Ile Glu Glu Asn Arg				
210		215		220
Leu Tyr Glu Lys Phe Asp Pro Arg Leu Pro Gly Lys Glu Pro Tyr Val				
225		230		235
Ser Ala Glu Pro Glu Val Thr Val Val Glu Leu Ser Gln Thr Leu Val				
	245		250	255
Pro Thr Glu Asp Asp Asp Phe Leu Ile Leu Ala Ser Asp Gly Leu Trp				
	260		265	270
Asp Val Leu Ser Asn Gln Glu Ala Val Asp Ile Val Arg Lys His Leu				
	275		280	285
Arg Lys Gly Asp Asp Lys Glu Val Lys Ser Ala Ala Gln Glu Leu Ala				
290		295		300
Arg Ala Asp Ser Leu Arg Ser Lys Lys His Asn Asp Pro Lys Glu Ala				
305		310		315
Ala Lys Leu Leu Val Asp Leu Ala Leu Lys Asp Asn Ile Thr Val Val				
	325		330	335
Val Val				

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